

Ellen J. Kapinos  
Genetics Institute Inc.  
87 CambridgePark Drive  
Cambridge, MA 02140

Randal J. Kaufman  
07/621,092  
November 30, 1990

JAN 18 1991

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS  
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE  
DISCLOSURES**

#2

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with one or more of the requirements of 37 CFR §§ 1.821 through 1.825 as follows:

- ☐ 1. This application clearly fails to comply with the collective requirements of §§ 1.821 through 1.825. Applicant's attention is directed to these regulations, a copy of which is attached.
- ☐ 2. This application does not conform exclusively to the requirements of §§ 1.821 through 1.825. The non-conforming material should be deleted. § 1.821(b).
- ☐ 3. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." § 1.821(c).
- ☐ 4. This application does contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." However, the "Sequence Listing" does not comply with the requirements of §§ 1.821 through 1.825 as follows:
  - ☐ a. The sequence data does not comply with the symbol and format requirements of paragraphs (b) through (p) of § 1.822. Specifically: \_\_\_\_\_
  - ☐ b. The "Sequence Listing" does not comply with the location and page requirements of paragraph (a) of § 1.823.
  - ☐ c. The "Sequence Listing" does not comply with the information requirements of paragraph (b) of § 1.823. Specifically: \_\_\_\_\_
  - ☐ d. Other: \_\_\_\_\_
- ☐ 5. The description and/or claims of the patent application mention a sequence that is set forth in the "Sequence Listing" but reference is not properly made to the sequence by use of a sequence identifier as required by § 1.821(d).
- ☐ 6. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by § 1.821(e).
- ☒ 7. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the computer readable form does not comply with the requirements of § 1.824. Specifically: SEE ATTACHED "RAW SEQUENCE LISTING".
- ☐ 8. A statement that the content of the paper and computer readable copies are the same has not been submitted as required by § 1.821(f).
- ☐ 9. The amendment to or replacement of the paper and/or computer readable copies of the "Sequence Listing" does not comply with the requirements of § 1.825(a) through (c).
- ☐ 10. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable. Applicant must provide a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. § 1.825(d). Specifically: \_\_\_\_\_
- ☐ 11. Other: \_\_\_\_\_

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE ABOVE REQUIREMENTS. Failure to comply with the above requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR § 1.136. Direct the response to, and any questions about, this notice to the undersigned. A copy of this notice MUST be returned with your response.

*Dora Straud*  
For: Manager, Application Processing Division  
(703) 303-1202 or 303-1203

☐ Examining Group  
(03) 308-

#6

**Raw Sequence Listing**  
**Patent Application US/07/621,092A**

01/24/91  
08:57:44

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kaufman, Randal J.  
Wasley, Louise

(ii) TITLE OF INVENTION: Method of Increasing Yield of  
Mature Proteins

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: Massachusetts  
(E) COUNTRY: United States of America  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage  
(B) COMPUTER: IBM PS/2  
(C) OPERATING SYSTEM: PC-DOS  
(D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 07/621092  
(B) FILING DATE: 26-NOV-1990  
(C) CLASSIFICATION: 424

(vii) PRIOR APPLICATION DATA: not applicable

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: Ellen J. Kapinos, Esquire  
(B) REGISTRATION NUMBER: 32,245  
(C) REFERENCE/DOCKET NUMBER: GI 5181

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54 (ix) TELECOMMUNICATION INFORMATION:  
55  
56 (A) TELEPHONE: (617) 876-1170  
57 (B) TELEFAX: (617) 876-5851  
58  
59 (2) INFORMATION FOR SEQ ID NO:1  
60  
61 (i) SEQUENCE CHARACTERISTICS:  
62  
63 (A) LENGTH: 2385 base pairs  
64  
65 (B) TYPE: nucleic acid  
66  
67 (C) STRANDEDNESS: double  
68  
69 (D) Topology: unknown  
70  
71 (ii) MOLECULE TYPE: partial human genomic DNA  
72  
73 (A) DESCRIPTION: sequence encoding furin  
74  
75 (iii) HYPOTHETICAL: no  
76  
77 (iv) ANTI-SENSE: no  
78  
79 (v) PUBLICATION INFORMATION: A.M.W. van den Ouweland et  
80 al, Nucl. Acids. Res., 18:664 (1990)  
81  
82 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:1  
83  
84 ATG GAG CTC AGG CCC TGG TTC 21  
85 Met Glu Leu Arg Pro Trp Leu  
86 1 5  
87  
88 CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA 60  
89 Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu  
90 10 15 20  
91  
92 GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG 99  
93 Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr  
94 25 30  
95  
96 TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC 138  
97 Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn  
98 35 40 45  
99  
100  
101 AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG 177  
102 Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln  
103 50 55  
104  
105 ATC TTC GGG GAC TAT TAC CAC TTC TGG CAT CGA GGA GTG 216  
106 Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val

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	60	65	70	
107				
108				
109				
110	ACG AAG CGG TCC CTG TCG CCT CAC CGC CCG CGG CAC AGC			255
111	Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser			
112	75	80	85	
113				
114				
115	CGG CTG CAG AGG GAG CCT CAA GTA CAG TGG CTG GAA CAG			294
116	Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln			
117	90	95		
118				
119	CAG GTG GCA AAG CGA CGG ACT AAA CGG GAC GTG TAC CAG			333
120	Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln			
121	100	105	110	
122				
123	GAG CCC ACA GAC CCC AAG TTT CCT CAG CAG TGG TAC CTG			372
124	Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu			
125	115	120		
126				
127	TCT GGT GTC ACT CAG CGG GAC CTG AAT GTG AAG GCG GCC			411
128	Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala			
129	125	130	135	
130				
131	TGG GCG CAG GGC TAC ACA GGG CAC GGC ATT CTG GTC TCC			450
132	Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser			
133	140	145	150	
134				
135	ATT CTG GAC GAT GGC ATC GAG AAG AAC CAC CCC GAC TTG			489
136	Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu			
137	155	160		
138				
139	GCA GGC AAT TAT GAT CCT GGG GCC AGT TTT CAT GTC AAT			528
140	Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn			
141	165	170	175	
142				
143	GAC CAG GAC CCT GAC CCC CAG CCT CGG TAC ACA CAG ATG			567
144	Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met			
145	180	185		
146				
147	AAT GAC AAC AGG CAC GGC ACA CGG TGT GCG GGG GAA GTG			606
148	Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val			
149	190	195	200	
150				
151	GCT GCC GTG GCC AAC AAC CGT GTC TGT GGT GTA GGT GTG			645
152	Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val			
153	205	210	215	
154				
155	GCC TAC AAC GCC CGC ATT GGA GGG GTC CGC ATG CTG GAT			684
156	Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp			
157	220	225		
158				
159	GGC GAG GTG ACA GAT GCA GTG GAG GCA CGC TCG CTG GGC			723

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160	Gly	Glu	Val	Thr	Asp	Ala	Val	Glu	Ala	Arg	Ser	Leu	Gly	
161		230					235					240		
162														
163	CTG	AAC	CCC	AAC	CAC	ATC	CAC	ATC	TAC	AGT	GCC	AGC	TGG	762
164	Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp	
165				245					250					
166														
167	GGC	CCC	GAG	GAT	GAC	GGC	AAG	ACA	GTG	GAT	GGG	CCA	GCC	801
168	Gly	Pro	Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala	
169	255					260					265			
170														
171	CGG	CTC	GCC	GAG	GAG	GCC	TTC	TTC	CGT	GGG	CTT	AGC	CAG	840
172	Arg	Leu	Ala	Glu	Glu	Ala	Phe	Phe	Arg	Gly	Val	Ser	Gln	
173			270					275					280	
174														
175	GGC	CGA	GGG	GGG	CTG	GGC	TCC	ATC	TTT	GTC	TGG	GCC	TCG	879
176	Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	Phe	Val	Trp	Ala	Ser	
177					285					290				
178														
179	GGG	AAC	GGG	GGG	CGG	GAA	CAT	GAC	AGC	TGC	AAC	TGC	GAC	918
180	Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	Cys	Asp	
181		295					300					305		
182														
183	GGC	TAC	ACC	AAC	AGT	ATC	TAC	ACG	CTG	TCC	ATC	AGC	AGC	957
184	Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser	
185				310					315					
186														
187	GCC	ACG	CAG	TTT	GGC	AAC	GTG	CCG	TGG	TAC	AGC	GAG	GCC	996
188	Ala	Thr	Gln	Phe	Gly	Asn	Val	Pro	Trp	Tyr	Ser	Glu	Ala	
189	320					325					330			
190														
191	TGC	TCG	TCC	ACA	CTG	GCC	ACG	ACC	TAC	AGC	AGT	GGC	AAC	1035
192	Cys	Ser	Ser	Thr	Leu	Ala	Thr	Thr	Tyr	Ser	Ser	Gly	Asn	
193			335					340					345	
194														
195	CAG	AAT	GAG	AAG	CAG	ATC	GTG	ACG	ACT	GAC	TTG	CGG	CAG	1074
196	Gln	Asn	Glu	Lys	Gln	Ile	Val	Thr	Thr	Asp	Leu	Arg	Gln	
197					350					355				
198														
199	AAG	TGC	ACG	GAG	TCT	CAC	ACG	GGC	ACC	TCA	GCC	TCT	GCC	1113
200	Lys	Cys	Thr	Glu	Ser	His	Thr	Gly	Thr	Ser	Ala	Ser	Ala	
201		360					365				370			
202														
203	CCC	TTA	GCA	GCC	GGC	ATC	ATT	GCT	CTC	ACC	CTG	GAG	GCC	1152
204	Pro	Leu	Ala	Ala	Gly	Ile	Ile	Ala	Leu	Thr	Leu	Glu	Ala	
205				375					380					
206														
207	AAT	AAG	AAC	CTC	ACA	TGG	CGG	GAC	ATG	CAA	CAC	CTG	GTG	1191
208	Asn	Lys	Asn	Leu	Thr	Trp	Arg	Asp	Met	Gln	His	Leu	Val	
209	385					390					395			
210														
211	GTA	CAG	ACC	TCG	AAG	CCA	GCC	CAC	CTC	AAT	GCC	AAC	GAC	1230
212	Val	Gln	Thr	Ser	Lys	Pro	Ala	His	Leu	Asn	Ala	Asn	Asp	

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	400	405	410	
213				
214				
215	TGG GCC ACC AAT GGT GTG GGG CGG AAA GTG AGC CAC TCA			1269
216	Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser			
217		415	420	
218				
219	TAT GGC TAC GGG CTT TTC GAC GCA GGC GCC ATG GTG GCC			1308
220	Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala			
221	425	430	435	
222				
223	CTG GCC CAG AAT TGG ACC ACA GTC GCC CCC CAG CGG AAG			1347
224	Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys			
225	440	445		
226				
227	TGC ATC ATC GAC ATC CTC ACC GAG CCC AAA GAC ATC GGG			1386
228	Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly			
229	450	455	460	
230				
231	AAA CGG CTC GAC CTC CGG AAC ACC GTG ACC GCG TCC CTG			1425
232	Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu			
233	465	470	475	
234				
235	GGC GAG CCC AAC CAC ATC ACT CGG CTG GAG CAC GCT CAG			1464
236	Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln			
237	480	485		
238				
239	GCG CGG CTC ACC CTG TCC TAT AAT CGC CGT GGC GAC CTG			1503
240	Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu			
241	490	495	500	
242				
243	GCC ATC CAC CTG GTC AGC CCC ATG GGC ACC CGC TCC ACC			1542
244	Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr			
245	505	510		
246				
247	CTG CTG GCA GCC AGG CCA CAT GAC TAC TCC GCA GAT GGG			1581
248	Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly			
249	515	520	525	
250				
251	TTT AAT GAC TGG GCC TTC ATG ACA ACT CAT TCC TGG GAT			1620
252	Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp			
253	530	535	540	
254				
255	GAC GAT CCC TCT GGG GAG TGG GTC CTA GAG ATT GAA AAC			1659
256	Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn			
257	545	550		
258				
259	ACC AGC GAA GCC AAC AAC TAT GGG ACG CTG ACC AAC TCC			1698
260	Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe			
261	555	560	565	
262				
263	ACC CTC GTA CTC TAT GGC ACC GCC CCT GAC GGG CTC CCC			1737
264	Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro			
265	570	575		

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266
267  GTA CCT CCA GAA AGC AGT GGC TGC AAG ACC CTC ACG TCC 1776
268  Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
269  580                      585                      590
270
271  AGT CAG GCC TGT GTG GTG TGC GAG GAA GGC TTC TCC CTC 1815
272  Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
273          595                      600                      605
274
275  CAC CAG AAG AGC TGT GTC CAG CAC TGC CCT CCA GGC TTC 1854
276  His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
277          610                      615
278
279  GCC CCC CAA GTC CTC GAT ACG CAC TAT AGC ACC GAG AAT 1893
280  Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
281          620                      625                      630
282
283  GAC GTG GAG ACC ATC CGG GCC AGC GTC TGC GCC CCC TGC 1932
284  Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
285          635                      640
286
287  CAC GCC TCA TGT GCC ACA TGC CAG GGG CCG GCC CTG ACA 1971
288  His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
289  645                      650                      655
290
291  GAC TGC CTC AGC TGC CCC AGC CAC GCC TCC TTG GAC CCT 2010
292  Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
293          660                      665                      670
294
295  GTG GAG CAG ACT TGC TCC CGG CAA AGC CAG AGC AGC CGA 2049
296  Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
297          675                      680
298
299  GAG TCC CCG CCA CAG CAG CAG CCA CCT CGG CTG CCC CCG 2088
300  Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
301          685                      690                      695
302
303  GAG GTG GAG GCG GGG CAA CGG CTG CGG GCA GGG CTG CTG 2127
304  Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
305          700                      705
306
307  CCC TCA CAC CTG CCT GAG GTG GTG GCC GGC CTC AGC TGC 2166
308  Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
309  710                      715                      720
310
311  GCC TTC ATC GTG CTG GTC TTC GTC ACT GTC TTC CTG CTC 2205
312  Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
313          725                      730                      735
314
315  CTG CAG CTG CGC TCT GGC TTT AGT TTT CGG GGG GTG AAG 2244
316  Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
317          740                      745
318

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319 GTG TAC ACC ATG GAC CGT GGC CTC ATC TCC TAC AAG GGG 2283  
 320 Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly  
 321 750 755 760

323 CTG CCC CCT GAA GCC TGG CAG GAG GAG TGC CCG TCT GAC 2322  
 324 Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp  
 325 765 770

327 TCA GAA GAG GAC GAG GGC CGG GGC GAG AGG ACC GCC TTT 2361  
 328 Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe  
 329 775 780 785

331 ATC AAA GAC CAG AGC GCC CTC TGA 2385  
 332 Ile Lys Asp Gln Ser Ala Leu End  
 333 790

## (3) INFORMATION FOR SEQ ID NO:2

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 amino acids

(B) TYPE: amino acids

(C) STRANDEDNESS: single

(D) Topology: unknown

(ii) MOLECULE TYPE: furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION: A.M.W. van den Ouweland et al,  
 Nucl. Acids. Res., 18:664 (1990)

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

360 Met Glu Leu Arg Pro Trp Leu  
 361 1 5

363 Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu  
 364 10 15 20

366 Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr  
 367 25 30

369 Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn  
 370 35 40 45

371



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372 Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln  
373 50 55  
374  
375 Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val  
376 60 65 70  
377  
378 Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser  
379 75 80 85  
380  
381  
382 Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln  
383 90 95  
384  
385 Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln  
386 100 105 110  
387  
388 Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu  
389 115 120  
390  
391 Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala  
392 125 130 135  
393  
394 Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser  
395 140 145 150  
396  
397 Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu  
398 155 160  
399  
400 Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn  
401 165 170 175  
402  
403 Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met  
404 180 185  
405  
406 Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val  
407 190 195 200  
408  
409 Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val  
410 205 210 215  
411  
412 Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp  
413 220 225  
414  
415 Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly  
416 230 235 240  
417  
418 Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp  
419 245 250  
420  
421 Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala  
422 255 260 265  
423  
424 Arg Leu Ala Glu Glu Ala Phe Phe Arg Gly Val Ser Gln

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425                    270                    275                    280  
426  
427 Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser  
428                    285                    290  
429  
430 Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp  
431                    295                    300                    305  
432  
433 Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser  
434                    310                    315  
435  
436  
437 Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala  
438 320                    325                    330  
439  
440 Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn  
441                    335                    340                    345  
442  
443 Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln  
444                    350                    355  
445  
446 Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala  
447                    360                    365                    370  
448  
449 Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala  
450                    375                    380  
451  
452 Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val  
453 385                    390                    395  
454  
455 Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp  
456                    400                    405                    410  
457  
458 Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser  
459                    415                    420  
460  
461 Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala  
462                    425                    430                    435  
463  
464 Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys  
465                    440                    445  
466  
467 Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly  
468 450                    455                    460  
469  
470 Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu  
471                    465                    470                    475  
472  
473 Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln  
474                    480                    485  
475  
476 Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu  
477                    490                    495                    500

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478  
479 Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr  
480 505 510  
481  
482 Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly  
483 515 520 525  
484  
485 Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp  
486 530 535 540  
487  
488 Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn  
489 545 550  
490  
491 Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe  
492 555 560 565  
493  
494 Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro  
495 570 575  
496  
497 Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser  
498 580 585 590  
499  
500 Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu  
501 595 600 605  
502  
503 His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe  
504 610 615  
505  
506 Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn  
507 620 625 630  
508  
509 Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys  
510 635 640  
511  
512 His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr  
513 645 650 655  
514  
515 Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro  
516 660 665 670  
517  
518 Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg  
519 675 680  
520  
521 Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro  
522 685 690 695  
523  
524 Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu  
525 700 705  
526  
527 Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys  
528 710 715 720  
529  
530 Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val

## Patent Application US/07/621,092A

531	725	730	735
532			
533	Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys		
534	740	745	
535			
536	Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly		
537	750	755	760
538			
539	Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp		
540	765	770	
541			
542	Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe		
543	775	780	785
544			
545			
546	Ile Lys Asp Gln Ser Ala Leu		
547	790		

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SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/621,092

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LINE ERROR

ORIGINAL TEXT

36 Wrong application Serial Number  
38 Wrong Filing Date  
40 Wrong Classification  
80 Extra Level-0 Records  
355 Extra Level-0 Records

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(C) CLASSIFICATION: 424  
al, Nucl. Acids. Res., 18:664 (1990)  
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CORRECTED TEXT

48 (viii) ATTORNEY/AGENT INFORMATION  
59 (2) INFORMATION FOR SEQ ID NO:1  
82 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:1  
336 (3) INFORMATION FOR SEQ ID NO:2  
357 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

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